SEQ ID NO: 1 Sequence Comparison A

```
LOCUS       HSFGFR                  2733 bp    mRNA    linear   PRI 23-MAR-1995
DEFINITION  Human mRNA for fibroblast growth factor (FGF) receptor.
ACCESSION   X51803
VERSION     X51803.1  GI:31367
KEYWORDS       FGF receptor; FGF receptor gene; fibroblast growth factor
receptor;
            FLG gene; receptor; transmembrane protein; tyrosine kinase.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2733)
  AUTHORS   Isacchi,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-FEB-1990) Isacchi A., Farmitalia Carlo Erba,
            Vialebezzi 24, 20146 Milano, Italy
REFERENCE   2  (bases 1 to 2733)
  AUTHORS   Isacchi,A., Bergonzoni,L. and Sarmientos,P.
  TITLE     Complete sequence of a human receptor for acidic and basic
            fibroblast growth factors
  JOURNAL   Nucleic Acids Res. 18 (7), 1906 (1990)
  MEDLINE   90245600
FEATURES             Location/Qualifiers
     source          1. .2733
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /tissue_type="placental"
                     /clone_lib="lambda gt11"
     sig_peptide     118. .180
     CDS             118. .2586
                     /note="precursor polypeptide (AA -21 to 801)"
                     /codon_start=1
                     /protein_id="CAA36101.1"
                     /db_xref="GI:31368"
                     /db_xref="SWISS-PROT:P11362"

/translation="MWSWKCLLFWAVLVTATLCTARPSPTLPEQAQPWGAPVEVESFL
VHPGDLLQLRCRLRDDVQSINWLRDGVQLAESNRTRITGEEVEVQDSVPADSGLYACV
TSSPSGSDTTYFSVNVSDALPSSEDDDDDDDSSSEEKETDNTKPNRMPVAPYWTSPEK
MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMD
SVVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFM
CKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFE
DAGEYTCLAGNSIGLSHHSAWLTVLEALEERPAVMTSPLYLEIIIYCTGAFLISCMVG
SVIVYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLS
SSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRV
TKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYASK
GNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIHRDL
AARNVLVTEDNVMKIADFGLARDIHHIDYYKKTTNGRLPVKWMAPEALFDRIYTHQSD
VWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAV
PSQRPTFKQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSFPDTRSSTCSSGEDSVFSH
EPLPEEPCLPRHPAQLANRGLKRR"
     mat_peptide     181. .2583
                     /product="FGF receptor mature peptide (AA 1 to 801)"
BASE COUNT      623 a    810 c    765 g    533 t      2 others
ORIGIN
```

```
alignment_scores:
            Quality: 4328.00              Length:    822
              Ratio:  5.284                Gaps:      1
 Percent Similarity:  99.635   Percent Identity: 99.513

alignment_block:
 US-09-620-561-1 x HSFGFR   ..

 Align seg 1/1  to: HSFGFR  from: 1  to: 2733

       1 MetTrpSerTrpLysCysLeuLeuPheTrpAlaValLeuValThrAlaTh 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     118 ATGTGGAGCTGGAAGTGCCTCCTCTTCTGGGCTGTGCTGGTCACAGCCAC 167

      17 rLeuCysThrAlaArgProSerProThrLeuProGluGlnAlaGlnProT 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     168 ACTCTGCACCGCTAGGCCGTCCCCGACCTTGCCTGAACAAGCCCAGCCCT 217

      34 rpGlyAlaProValGluValGluSerPheLeuValHisProGlyAspLeu 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     218 GGGGAGCCCCTGTGGAAGTGGAGTCCTTCCTGGTCCACCCCGGTGACCTG 267

      51 LeuGlnLeuArgCysArgLeuArgAspAspValGlnSerIleAsnTrpLe 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     268 CTGCAGCTTCGCTGTCGGCTGCGGGACGATGTGCAGAGCATCAACTGGCT 317

      67 uArgAspGlyValGlnLeuAlaGluSerAsnArgThrArgIleThrGlyG 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     318 GCGGGACGGGGTGCAGCTGGCGGAAAGCAACCGCACCCGCATCACAGGGG 367

      84 luGluValGluValGlnAspSerValProAlaAspSerGlyLeuTyrAla 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     368 AGGAGGTGGAGGTGCAGGACTCCGTGCCCGCAGACTCCGGCCTCTATGCT 417

     101 CysValThrSerSerProSerGlyLysAspThrThrTyrPheSerValAs 117
         ||||||||||||||||||||||:::||||||||||||||||||||||||
     418 TGCGTAACCAGCAGCCCCTCGGGCAGTGACACCACCTACTTCTCCGTCAA 467

     117 nValSerAspAlaLeuProSerSerGluAspAspAspAspAspAspAspS 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     468 TGTTTCAGATGCTCTCCCCTCCTCGGAGGATGATGATGATGATGACT 517

     134 erSerSerGluGluLysGluThrAspAsnThrLysProAsn......Pro 148
         ||||||||||||||||||||||||||||||||||||||||      |||
     518 CCTCTTCAGAGGAGAAAGAAACAGATAACACCAAACCAAACCGTATGCCC 567

     149 ValAlaProTyrTrpThrSerProGluLysMetGluLysLysLeuHisAl 165
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     568 GTAGCTCCATATTGGACATCCCCAGAAAAGATGGAAAAGAAATTGCATGC 617

     165 aValProAlaAlaLysThrValLysPheLysCysProSerSerGlyThrP 182
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     618 AGTGCCGGCTGCCAAGACAGTGAAGTTCAAATGCCCTTCCAGTGGGACCC 667

     182 roAsnProThrLeuArgTrpLeuLysAsnGlyLysGluPheLysProAsp 198
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     668 CAAACCCCACACTGCGCTGGTTGAAAAATGGCAAAGAATTCAAACCTGAC 717
```

```
 199 HisArgIleGlyGlyTyrLysValArgTyrAlaThrTrpSerIleIleMe 215
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 718 CACAGAATTGGAGGCTACAAGGTCCGTTATGCCACCTGGAGCATCATAAT 767

 215 tAspSerValValProSerAspLysGlyAsnTyrThrCysIleValGluA 232
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 768 GGACTCTGTGGTGCCCTCTGACAAGGGCAACTACACCTGCATTGTGGAGA 817

 232 snGluTyrGlySerIleAsnHisThrTyrGlnLeuAspValValGluArg 248
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 818 ATGAGTACGGCAGCATCAACCACACATACCAGCTGGATGTCGTGGAGCGG 867

 249 SerProHisArgProIleLeuGlnAlaGlyLeuProAlaAsnLysThrVa 265
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 868 TCCCCTCACCGGCCCATCCTGCAAGCAGGGTTGCCCGCCAACAAAACAGT 917

 265 lAlaLeuGlySerAsnValGluPheMetCysLysValTyrSerAspProG 282
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 918 GGCCCTGGGTAGCAACGTGGAGTTCATGTGTAAGGTGTACAGTGACCCGC 967

 282 lnProHisIleGlnTrpLeuLysHisIleGluValAsnGlySerLysIle 298
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 968 AGCCGCACATCCAGTGGCTAAAGCACATCGAGGTGAATGGGAGCAAGATT 1017

 299 GlyProAspAsnLeuProTyrValGlnIleLeuLysThrAlaGlyValAs 315
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1018 GGCCCAGACAACCTGCCTTATGTCCAGATCTTGAAGACTGCTGGAGTTAA 1067

 315 nThrThrAspLysGluMetGluValLeuHisLeuArgAsnValSerPheG 332
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1068 TACCACCGACAAAGAGATGGAGGTGCTTCACTTAAGAAATGTCTCCTTTG 1117

 332 luAspAlaGlyGluTyrThrCysLeuAlaGlyAsnSerIleGlyLeuSer 348
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1118 AGGACGCAGGGGAGTATACGTGCTTGGCGGGTAACTCTATCGGACTCTCC 1167

 349 HisHisSerAlaTrpLeuThrValLeuGluAlaLeuGluGluArgProAl 365
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1168 CATCACTCTGCATGGTTGACCGTTCTGGAAGCCCTGGAAGAGAGGCCGGC 1217

 365 aValMetThrSerProLeuTyrLeuGluIleIleIleTyrCysThrGlyA 382
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1218 AGTGATGACCTCGCCCCTGTACCTGGAGATCATCATCTATTGCACAGGGG 1267

 382 laPheLeuIleSerCysMetValGlySerValIleValTyrLysMetLys 398
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1268 CCTTCCTCATCTCCTGCATGGTGGGGTCGGTCATCGTCTACAAGATGAAG 1317

 399 SerGlyThrLysLysSerAspPheHisSerGlnMetAlaValHisLysLe 415
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1318 AGTGGTACCAAGAAGAGTGACTTCCACAGCCAGATGGCTGTGCACAAGCT 1367

 415 uAlaLysSerIleProLeuArgArgGlnValThrValSerAlaAspSerS 432
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1368 GGCCAAGAGCATCCCTCTGCGCAGACAGGTAACAGTGTCTGCTGACTCCA 1417
```

```
 432 erAlaSerMetAsnSerGlyValLeuLeuValArgProSerArgLeuSer 448
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1418 GTGCATCCATGAACTCTGGGGTTCTTCTGGTTCGGCCATCACGGCTCTCC 1467

 449 SerSerGlyThrProMetLeuAlaGlyValSerGluTyrGluLeuProGl 465
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1468 TCCAGTGGGACTCCCATGCTAGCAGGGGTCTCTGAGTATGAGCTTCCCGA 1517

 465 uAspProArgTrpGluLeuProArgAspArgLeuValLeuGlyLysProL 482
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1518 AGACCCTCGCTGGGAGCTGCCTCGGGACAGACTGGTCTTAGGCAAACCCC 1567

 482 euGlyGluGlyCysPheGlyGlnValValLeuAlaGluAlaIleGlyLeu 498
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1568 TGGGAGAGGGCTGCTTTGGGCAGGTGGTGTTGGCAGAGGCTATCGGGCTG 1617

 499 AspLysAspLysProAsnArgValThrLysValAlaValLysMetLeuLy 515
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1618 GACAAGGACAAACCCAACCGTGTGACCAAAGTGGCTGTGAAGATGTTGAA 1667

 515 sSerAspAlaThrGluLysAspLeuSerAspLeuIleSerGluMetGluM 532
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1668 GTCGGACGCAACAGAGAAAGACTTGTCAGACCTGATCTCAGAAATGGAGA 1717

 532 etMetLysMetIleGlyLysHisLysAsnIleIleAsnLeuLeuGlyAla 548
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1718 TGATGAAGATGATCGGGAAGCATAAGAATATCATCAACCTGCTGGGGGCC 1767

 549 CysThrGlnAspGlyProLeuTyrValIleValGluTyrAlaSerLysGl 565
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1768 TGCACGCAGGATGGTCCCTTGTATGTCATCGTGGAGTATGCCTCCAAGGG 1817

 565 yAsnLeuArgGluTyrLeuGlnAlaArgArgProProGlyLeuGluTyrC 582
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1818 CAACCTGCGGGAGTACCTGCAGGCCCGGAGGCCCCCAGGGCTGGAATACT 1867

 582 ysTyrAsnProSerHisAsnProGluGluGlnLeuSerSerLysAspLeu 598
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1868 GCTACAACCCCAGCCACAACCCAGAGGAGCAGCTCTCCTCCAAGGACCTG 1917

 599 ValSerCysAlaTyrGlnValAlaArgGlyMetGluTyrLeuAlaSerLy 615
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1918 GTGTCCTGCGCCTACCAGGTGGCCCGAGGCATGGAGTATCTGGCCTCCAA 1967

 615 sLysCysIleHisArgAspLeuAlaAlaArgAsnValLeuValThrGluA 632
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1968 GAAGTGCATACACCGAGACCTGGCAGCCAGGAATGTCCTGGTGACAGAGG 2017

 632 spAsnValMetLysIleAlaAspPheGlyLeuAlaArgAspIleHisHis 648
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2018 ACAATGTGATGAAGATAGCAGACTTTGGCCTCGCACGGGACATTCACCAC 2067

 649 IleAspTyrTyrLysLysThrThrAsnGlyArgLeuProValLysTrpMe 665
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2068 ATCGACTACTATAAAAAGACAACCAACGGCCGACTGCCTGTGAAGTGGAT 2117
```

```
 665 tAlaProGluAlaLeuPheAspArgIleTyrThrHisGlnSerAspValT 682
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2118 GGCACCCGAGGCATTATTTGACCGGATCTACACCCACCAGAGTGATGTGT 2167

 682 rpSerPheGlyValLeuLeuTrpGluIlePheThrLeuGlyGlySerPro 698
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2168 GGTCTTTCGGGGTGCTCCTGTGGGAGATCTTCACTCTGGGCGGCTCCCCA 2217

 699 TyrProGlyValProValGluGluLeuPheLysLeuLeuLysGluGlyHi 715
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2218 TACCCCGGTGTGCCTGTGGAGGAACTTTTCAAGCTGCTGAAGGAGGGTCA 2267

 715 sArgMetAspLysProSerAsnCysThrAsnGluLeuTyrMetMetMetA 732
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2268 CCGCATGGACAAGCCCAGTAACTGCACCAACGAGCTGTACATGATGATGC 2317

 732 rgAspCysTrpHisAlaValProSerGlnArgProThrPheLysGlnLeu 748
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2318 GGGACTGCTGGCATGCAGTGCCCTCACAGAGACCCACCTTCAAGCAGCTG 2367

 749 ValGluAspLeuAspArgIleValAlaLeuThrSerAsnGlnGluTyrLe 765
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2368 GTGGAAGACCTGGACCGCATCGTGGCCTTGACCTCCAACCAGGAGTACCT 2417

 765 uAspLeuSerMetProLeuAspGlnTyrSerProSerPheProAspThrA 782
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2418 GGACCTGTCCATGCCCCTGGACCAGTACTCCCCCAGCTTTCCCGACACCC 2467

 782 rgSerSerThrCysSerSerGlyGluAspSerValPheSerHisGluPro 798
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2468 GGAGCTCTACGTGCTCCTCAGGGGAGGATTCCGTCTTCTCTCATGAGCCG 2517

 799 LeuProGluGluProCysLeuProArgHisProAlaGlnLeuAlaAsnGl 815
     ||||||||||||||||||||||||||||||||||||||||||||||||||
2518 CTGCCCGAGGAGCCCTGCCTGCCCCGACACCCAGCCCAGCTTGCCAATCG 2567

 815 yGlyLeuLysArgArg 820
      ||||||||||||||||
2568 GGGACTCAAACGCCGC 2583
```

Sequence Comparison B

```
FGR1_HUMAN
ID   FGR1_HUMAN     STANDARD;      PRT;   822 AA.
AC   P11362; P17049;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Basic fibroblast growth factor receptor 1 precursor (EC 2.7.1.112)
DE   (FGFR-1) (bFGF-R) (Fms-like tyrosine kinase-2) (c-fgr).
GN   FGFR1 OR FLG OR FGFBR OR FLT2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
```

RC TISSUE=Placenta;
RX MEDLINE=90245600; PubMed=2159626;
RA **Isacchi A., Bergonzoni L., Sarmientos P.;**
RT "Complete sequence of a human receptor for acidic and basic
RT fibroblast growth factors.";
RL Nucleic Acids Res. 18:1906-1906(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Neonatal brain stem;
RX MEDLINE=90360977; PubMed=1697263;
RA **Dionne C.A., Crumley G.R., Bellot F., Kaplow J.M., Searfoss G.,**
RA Ruta M., Burgess W.H., Jaye M., Schlessinger J.;
RT "Cloning and expression of two distinct high-affinity receptors
RT cross-reacting with acidic and basic fibroblast growth factors.";
RL EMBO J. 9:2685-2692(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92282615; PubMed=1317750;
RA Hattori Y., Odagiri H., Katoh O., Sakamoto H., Morita T.,
RA Shimotohno K., Tobinai K., Sugimura T., Terada M.;
RT "K-sam-related gene, N-sam, encodes fibroblast growth factor receptor
RT and is expressed in T-lymphocytic tumors.";
RL Cancer Res. 52:3367-3371(1992).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91126480; PubMed=1846977;
RA Hou J., Kan M., McKeehan K., McBride G., Adams P., McKeehan W.L.;
RT "Fibroblast growth factor receptors from liver vary in three
RT structural domains.";
RL Science 251:665-668(1991).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=92118399; PubMed=1662973;
RA Kiefer M.C., Baird A., George-Nascimento C., Nguyen T., Mason O.B.,
RA Boley L.J., Valenzuela P., Barr P.J.;
RT "Molecular cloning of a human basic fibroblast growth factor receptor
RT cDNA and expression of a biologically active extracellular domain in
RT a baculovirus system.";
RL Growth Factors 5:115-127(1991).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90290512; PubMed=2162671;
RA **Itoh N., Terachi T., Ohta M., Seo M.K.;**
RT "The complete amino acid sequence of the shorter form of human basic
RT fibroblast growth factor receptor deduced from its cDNA.";
RL Biochem. Biophys. Res. Commun. 169:680-685(1990).
RN [7]
RP SEQUENCE OF 201-822 FROM N.A.
RA **Ruta M., Howk R., Ricca G., Drohan W., Zabelshansky M., Laureys G.,**
RA Barton D.E., Francke U., Schlessinger J., Givol D.;
RT "A novel protein tyrosine kinase gene whose expression is modulated
RT during endothelial cell differentiation.";
RL Oncogene 3:9-15(1988).
RN [8]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

RX MEDLINE=90355989; PubMed=2167437;
RA **Johnson D.E., Lee P.L., Lu J., Williams L.T.;**
RT "Diverse forms of a receptor for acidic and basic fibroblast growth
RT factors.";
RL Mol. Cell. Biol. 10:4728-4736(1990).
RN [9]
RP ALTERNATIVE SPLICING.
RX MEDLINE=91141499; PubMed=1847500;
RA Gutkind S.J., Link D.C., Katamine S., Lacal P., Miki T., Ley T.J.,
RA Robbins K.C.;
RT "A novel c-fgr exon utilized in Epstein-Barr virus-infected B
RT lymphocytes but not in normal monocytes.";
RL Mol. Cell. Biol. 11:1500-1507(1991).
RN [10]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Lung;
RX MEDLINE=91319400; PubMed=1650441;
RA Eisemann A., Ahn J.A., Graziani G., Tronick S.R., Ron D.;
RT "Alternative splicing generates at least five different isoforms of
RT the human basic-FGF receptor.";
RL Oncogene 6:1195-1202(1991).
RN [11]
RP SEQUENCE FROM N.A.
RA Wennstroem S., Sandstroem C., Claesson-Welsh L.;
RL Submitted (JUL-1990) to the EMBL/GenBank/DDBJ databases.
RN [12]
RP MUTAGENESIS OF TYR-766.
RX MEDLINE=92357144; PubMed=1379697;
RA Peters K.G., Marie J., Wilson E., Ives H.E., Escobedo J.,
RA del Rosario M., Mirda D., Williams L.T.;
RT "Point mutation of an FGF receptor abolishes phosphatidylinositol
RT turnover and Ca2+ flux but not mitogenesis.";
RL Nature 358:678-681(1992).
RN [13]
RP MUTAGENESIS OF TYR-766.
RX MEDLINE=92357145; PubMed=1379698;
RA Mohammadi M., Dionne C.A., Li W., Lin N., Spivak T., Honegger A.M.,
RA Jaye M., Schlessinger J.;
RT "Point mutation in FGF receptor eliminates phosphatidylinositol
RT hydrolysis without affecting mitogenesis.";
RL Nature 358:681-684(1992).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 464-762.
RX MEDLINE=96361355; PubMed=8752212;
RA Mohammadi M., Schlessinger J., Hubbard S.R.;
RT "Structure of the FGF receptor tyrosine kinase domain reveals a novel
RT autoinhibitory mechanism.";
RL Cell 86:577-587(1996).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 464-762.
RX MEDLINE=97284786; PubMed=9139660;
RA Mohammadi M., McMahon G., Sun L., Tang C., Hirth P., Yeh B.K.,
RA Hubbard S.R., Schlessinger J.;
RT "Structures of the tyrosine kinase domain of fibroblast growth factor
RT receptor in complex with inhibitors.";
RL Science 276:955-960(1997).
RN [16]

```
RP   VARIANT PFEIFFER SYNDROME ARG-252.
RX   MEDLINE=95179173; PubMed=7874169;
RA   Muenke M., Schell U., Hehr A., Robin N.H., Losken H.W., Schinzel A.,
RA   Pulleyn L.J., Rutland P., Reardon W., Malcolm S., Winter R.M.;
RT   "A common mutation in the fibroblast growth factor receptor 1 gene in
RT   Pfeiffer syndrome.";
RL   Nat. Genet. 8:269-274(1994).
CC   -!- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR. A SHORTER
CC       FORM OF THE RECEPTOR COULD BE A RECEPTOR FOR ACIDIC FGF (AFGF).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS: MANY FORMS OF FGFR1 ARE PRODUCED BY
CC       ALTERNATIVE SPLICING. THE FORM SHOWN HERE IS KNOWN AS ALPHA-A1.
CC   -!- DISEASE: DEFECTS IN FGFR1 ARE ONE OF THE CAUSES OF PFEIFFER
CC       SYNDROME (FS) (ALSO KNOWN AS ACROCEPHALOSYNDACTYLY TYPE V; ACS5);
CC       CHARACTERIZED BY CRANIOSYNOSTOSIS (PREMATURE FUSION OF THE SKULL
CC       SUTURES) WITH DEVIATION AND ENLARGEMENT OF THE THUMBS AND GREAT
CC       TOES, BRACHYMESOPHALANGY, WITH PHALANGEAL ANKYLOSIS AND A VARYING
CC       DEGREE OF SOFT TISSUE SYNDACTYLY.
CC   -!- DISEASE: Involved in a t(8;13)(p12;q12) chromosomal translocation
CC       which involves FGFR1 AND ZNF198. The resulting transcript is a
CC       possible candidate for stem cell leukemia lymphoma syndrome/SCLL.
CC   -!- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR
CC       FAMILY.
CC   -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   ---------------------------------------------------------------------
--
CC   This SWISS-PROT entry is copyright. It is produced through a
collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation
-
CC   the European Bioinformatics Institute.  There are no  restrictions on
its
CC   use  by  non-profit  institutions as long  as its content  is  in  no
way
CC   modified and this statement is not removed.  Usage  by  and for
commercial
CC   entities requires a license agreement (See http://www.isb-
sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
--
DR   EMBL; X51803; CAA36101.1; -.
DR   EMBL; X52833; CAA37015.1; -.
DR   EMBL; X66945; CAA47375.1; -.
DR   EMBL; Y00665; CAA68679.1; -.
DR   EMBL; M37722; AAA75007.1; -.
DR   EMBL; M60485; AAA35840.1; -.
DR   EMBL; M63887; AAA35958.1; -.
DR   EMBL; M34185; AAA35836.1; -.
DR   EMBL; M34186; AAA35837.1; -.
DR   EMBL; X57118; CAA40400.1; ALT_TERM.
DR   EMBL; X57119; CAA40401.1; -.
DR   EMBL; X57120; CAA40402.1; -.
DR   EMBL; X57121; CAA40403.1; -.
DR   EMBL; X57122; CAA40404.1; -.
```

```
DR   EMBL; M34641; AAA35835.1; -.
DR   EMBL; A29216; CAA01958.1; -.
DR   PIR; S11692; TVHUFG.
DR   PIR; S25420; S25420.
DR   PIR; S26739; S26739.
DR   PDB; 1FGK; 23-JUL-97.
DR   PDB; 1FGI; 08-APR-98.
DR   PDB; 1AGW; 25-MAR-98.
DR   MIM; 136350; -.
DR   MIM; 101600; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00047; ig; 3.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   SMART; SM00408; IGc2; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;

  Query Match             99.6%;  Score 4336;  DB 1;  Length 822;
  Best Local Similarity   99.6%;  Pred. No. 3e-259;
  Matches  819;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps
1;

Qy       1 MWSWKCLLFWAVLVTATLCTARPSPTLPEQAQPWGAPVEVESFLVHPGDLLQLRCRLRDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MWSWKCLLFWAVLVTATLCTARPSPTLPEQAQPWGAPVEVESFLVHPGDLLQLRCRLRDD 60

Qy      61 VQSINWLRDGVQLAESNRTRITGEEVEVQDSVPADSGLYACVTSSPSGKDTTYFSVNVSD 120
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      61 VQSINWLRDGVQLAESNRTRITGEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVSD 120

Qy     121 ALPSSEDDDDDDDSSSEEKETDNTKPN--PVAPYWTSPEKMEKKLHAVPAAKTVKFKCPS 178
           |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db     121 ALPSSEDDDDDDDSSSEEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPS 180

Qy     179 SGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSIN 238
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 SGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSIN 240

Qy     239 HTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKI 298
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 HTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKI 300

Qy     299 GPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE 358
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE 360

Qy     359 ALEERPAVMTSPLYLEIIIYCTGAFLISCMVGSVIVYKMKSGTKKSDFHSQMAVHKLAKS 418
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ALEERPAVMTSPLYLEIIIYCTGAFLISCMVGSVIVYKMKSGTKKSDFHSQMAVHKLAKS 420
```

```
Qy    419 IPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVL 478
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 IPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVL 480

Qy    479 GKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGK 538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGK 540

Qy    539 HKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDL 598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 HKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDL 600

Qy    599 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKTTNG 658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKTTNG 660

Qy    659 RLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKEGHRMD 718
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 RLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKEGHRMD 720

Qy    719 KPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSF 778
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 KPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSF 780

Qy    779 PDTRSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR 820
          |||||||||||||||||||||||||||||||||||||||||||
Db    781 PDTRSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR 822
```

Sequence Comparison C

HUMFGF5H/c

SEQ ID NO:7

```
LOCUS       HUMFGF5H                1625 bp    mRNA    linear   PRI 27-APR-1993
DEFINITION Human fibroblast growth factor receptor (FGFr) secreted form mRNA,
           complete cds.
ACCESSION   M34188
VERSION     M34188.1  GI:182546
KEYWORDS    FGF receptor; fibroblast growth factor receptor.
SOURCE      Human female placenta endothelial cell line HUVEC, cDNA to mRNA,
           clone h5.
  ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1625)
  AUTHORS   Johnson,D.E., Lee,P.L., Lu,J. and Williams,L.T.
  TITLE     Diverse forms of a receptor for acidic and basic fibroblast growth
           factors
  JOURNAL   Mol. Cell. Biol. 10, 4728-4736 (1990)
  MEDLINE   90355989
COMMENT    Draft entry and computer-readable sequence for [Unpublished (1990)]
           kindly submitted
           by D.E.Johnson, 10-MAY-1990.
             Author address: D.E.Johnson
             University of California San Francisco
             4th and Parnassus
             Howard Hughes Medical Institute
             San Francisco, CA 94143
             (415) 476-4297.
FEATURES             Location/Qualifiers
     source          1. .1625
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             523. .1425
                     /note="fibroblast growth factor receptor (FGFr)
                     transmembrane form"
                     /codon_start=1
                     /protein_id="AAA35839.1"
                     /db_xref="GI:182547"

/translation="MWSWKCLLFWAVLVTATLCTARPSPTLPEQDALPSSEDDDDDDD
SSSEEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKN
GKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVERS
PHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQ
ILKVIMAPVFVGQSTGKETTVSGAQVPVGRLSCPRMGSFLTLQAHTLHLSRDLATSPR
TSNRGHKVEVSWEQRAAGMGGAGL"
BASE COUNT      368 a    480 c    489 g    288 t
ORIGIN

  Query Match             100.0%;  Score 30;  DB 9;  Length 1625;
  Best Local Similarity   100.0%;  Pred. No. 0.0028;
  Matches    30;  Conservative     0;  Mismatches     0;  Indels     0;  Gaps
0;

Qy       1 ataacggaccttgtagcctccaattctgtg 30
           ||||||||||||||||||||||||||||||
Db     879 ATAACGGACCTTGTAGCCTCCAATTCTGTG 850
```

Sequence Comparison D

```
LOCUS       HSFLGMR                 1974 bp    mRNA    linear   PRI 28-JUL-1995
DEFINITION   Human flg (fms-like gene) mRNA for putative protein tyrosine
kinase
            (partial).
ACCESSION   Y00665
VERSION     Y00665.1  GI:558583
KEYWORDS    tyrosine kinase.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1974)
  AUTHORS   Ruta,M., Howk,R., Ricca,G., Drohan,W., Zabelshansky,M., Laureys,G.,
            Barton,D.E., Francke,U., Schlessinger,J. and Givol,D.
TITLE     A novel protein tyrosine kinase gene whose expression is modulated
during endothelial cell differentiation
  JOURNAL   Oncogene 3, 9-15 (1988)
COMMENT     On Oct 18, 1994 this sequence version replaced gi:31427.
FEATURES             Location/Qualifiers
     source          1. .1974
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     mat_peptide     <1. .1866
                     /gene="flg"
                     /product="tyrosine kinase"
     source          1. .1971
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="8p12"
                     /clone="5"
                     /cell_type="endothelial"
                     /clone_lib="lambda-gt11"
     gene            1. .1869
                     /gene="flg"
     CDS             <1. .1869
                     /gene="flg"
                     /codon_start=1
                     /product="tyrosine kinase"
                     /protein_id="CAA68679.1"
                     /db_xref="GI:558584"
                     /db_xref="SWISS-PROT:P11362"

/translation="HRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQ
LDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGP
DNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE
ALEQRPAVMTSPLYLEIIIYCTGAFLISCMVGSVIVYKMKSGTKKSDFHSQMAVHKLA
KSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRD
RLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEM
MKMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPE
EQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHH
IDYYKKTTNGRLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEE
LFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEY
LDLSMPLDQYSPSFPDTRSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR"
BASE COUNT      449 a    587 c    548 g    390 t
ORIGIN
```

Query Match 100.0%; Score 30; DB 9; Length 1974;

Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 ataacggaccttgtagcctccaattctgtg 30
           ||||||||||||||||||||||||||||||
Db      30 ATAACGGACCTTGTAGCCTCCAATTCTGTG 1
```

SEQ ID NO:8 Sequence Comparison E

```
LOCUS       HSFLGMR                 1974 bp    mRNA    linear   PRI 28-JUL-1995
DEFINITION  Human flg (fms-like gene) mRNA for putative protein tyrosine
kinase
            (partial).
ACCESSION   Y00665
VERSION     Y00665.1  GI:558583
KEYWORDS    tyrosine kinase.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1974)
  AUTHORS   Ruta,M., Howk,R., Ricca,G., Drohan,W., Zabelshansky,M.,
Laureys,G.,
            Barton,D.E., Francke,U., Schlessinger,J. and Givol,D.
  TITLE     A novel protein tyrosine kinase gene whose expression is
modulated
            during endothelial cell differentiation
  JOURNAL   Oncogene 3, 9-15 (1988)
COMMENT     On Oct 18, 1994 this sequence version replaced gi:31427.
FEATURES             Location/Qualifiers
     source          1. .1974
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     mat_peptide     <1. .1866
                     /gene="flg"
                     /product="tyrosine kinase"
     source          1. .1971
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="8p12"
                     /clone="5"
                     /cell_type="endothelial"
                     /clone_lib="lambda-gt11"
     gene            1. .1869
                     /gene="flg"
     CDS             <1. .1869
                     /gene="flg"
                     /codon_start=1
                     /product="tyrosine kinase"
                     /protein_id="CAA68679.1"
                     /db_xref="GI:558584"
                     /db_xref="SWISS-PROT:P11362"
```

/translation="HRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQ
LDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGP
DNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE
ALEQRPAVMTSPLYLEIIIYCTGAFLISCMVGSVIVYKMKSGTKKSDFHSQMAVHKLA
KSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRD
RLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEM
MKMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPE
EQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHH
IDYYKKTTNGRLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEE
LFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEY
LDLSMPLDQYSPSFPDTRSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR"
BASE COUNT 449 a 587 c 548 g 390 t
ORIGIN

Query Match 100.0%; Score 30; DB 9; Length 1974;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcggcgtttgagtccgccattggcaagctg 30
||||||||||||||||||||||||||||||
Db 1866 GCGGCGTTTGAGTCCGCCATTGGCAAGCTG 1837

Sequence Comparison F

LOCUS HSFGFRFL 2662 bp mRNA linear PRI 23-MAR-1995
DEFINITION Human flg mRNA for fibroblast growth factor receptor-FLG.
ACCESSION X52833
VERSION X52833.1 GI:31377
KEYWORDS cell surface glycoprotein; fibroblast growth factor receptor; tyrosine kinase.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2662)
AUTHORS Dionne,C.A.
TITLE Direct Submission
JOURNAL Submitted (01-JUN-1990) Dionne C., Rorer Central Research, 680 Allelande Road, King of Prussia, PA 19425, USA
REFERENCE 2 (bases 1 to 2662)
AUTHORS **Dionne,C.A., Crumley,G., Bellot,F., Kaplow,J.M., Searfoss,G., Ruta,M., Burgess,W.H., Jaye,M. and Schlessinger,J.**
TITLE **Cloning and expression of two distinct high-affinity receptors cross-reacting with acidic and basic fibroblast growth factors**
JOURNAL **EMBO J. 9 (9), 2685-2692 (1990)**
MEDLINE 90360977
REFERENCE 3 (bases 1 to 2662)
AUTHORS Crumley,G., Bellot,F., Kaplow,J.M., Schlessinger,J., Jaye,M. and Dionne,C.A.
TITLE High-affinity binding and activation of a truncated FGF receptor by
both aFGF and bFGF
JOURNAL Oncogene 6 (12), 2255-2262 (1991)
MEDLINE 92115326
FEATURES Location/Qualifiers
source 1. .2662
/organism="Homo sapiens"

```
                     /db_xref="taxon:9606"
                     /cell_line="HUVEC"
                     /clone_lib="lambda gt11"
     sig_peptide     88. .150
     CDS             88. .2556
                     /note="fibroblast growth factor receptor-FLG precursor"
                     /codon_start=1
                     /protein_id="CAA37015.1"
                     /db_xref="GI:31378"
                     /db_xref="SWISS-PROT:P11362"

/translation="MWSWKCLLFWAVLVTATLCTARPSPTLPEQAQPWGAPVEVESFL
VHPGDLLQLRCRLRDDVQSINWLRDGVQLAESNRTRITGEEVEVQDSVPADSGLYACV
TSSPSGSDTTYFSVNVSDALPSSEDDDDDDDSSSEEKETDNTKPNRMPVAPYWTSPEK
MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMD
SVVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFM
CKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFE
DAGEYTCLAGNSIGLSHHSAWLTVLEALEERPAVMTSPLYLEIIIYCTGAFLISCMVG
SVIVYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLS
SSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRV
TKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYASK
GNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIHRDL
AARNVLVTEDNVMKIADFGLARDIHHIDYYKKTTNGRLPVKWMAPEALFDRIYTHQSD
VWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAV
PSQRPTFKQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSFPDTRSSTCSSGEDSVFSH
                     EPLPEEPCLPRHPAQLANGGLKRR"
     mat_peptide     151. .2553
                     /product="mature fibroblast growth factor receptor -FLG"
BASE COUNT      613 a    787 c    740 g    522 t
ORIGIN


  Query Match             100.0%;  Score 30;  DB 9;  Length 2662;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy      1 gcggcgtttgagtccgccattggcaagctg 30
          ||||||||||||||||||||||||||||||
Db   2553 GCGGCGTTTGAGTCCGCCATTGGCAAGCTG 2524
```

Sequence Comparison 6

```
DEFINITION  Human shorter form basic fibroblast growth factor (bFGF) receptor
            mRNA, complete cds.
ACCESSION   M37722
VERSION     M37722.1  GI:179413
KEYWORDS    fibroblast growth factor basic; receptor-like protein.
SOURCE      Homo sapiens placenta cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3328)
  AUTHORS   Itoh,N., Terachi,T., Ohta,M. and Seo,M.K.
  TITLE     The complete amino acid sequence of the shorter form of human
basic
            fibroblast growth factor receptor deduced from its cDNA
  JOURNAL   Biochem. Biophys. Res. Commun. 169 (2), 680-685 (1990)
```

```
  MEDLINE   90290512
FEATURES             Location/Qualifiers
     source          1. .3328
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /tissue_type="placenta"
     5'UTR           1. .228
sig_peptide     229. .288
     CDS             229. .2424
                     /note="precursor"
                     /codon_start=1
                     /product="basic fibroblast growth factor receptor
protein"
                     /protein_id="AAA75007.1"
                     /db_xref="GI:179415"

/translation="MWSWKCLLFWAVLVTATLCTARPSPTLPEQDALPSSEDDDDDDD
SSSEEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKN
GKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVERS
PHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQ
ILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLEALEERPA
VMTSPLYLEIIIYCTGAFLISCMVGSVIVYKMKSGTKKSDFHSQMAVHKLAKSIPLRR
QVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDLRWELPRDRLVLGKP
LGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKH
KNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKD
LVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKT
TNGRLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKE
GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEYLDLSMPL
DQYSPSFPDTRSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR"
     mat_peptide     289. .2421
/product="basic fibroblast growth factor receptor protein"
     3'UTR           2425. .3328
BASE COUNT      777 a    946 c    902 g    703 t
ORIGIN
```

```
  Query Match             100.0%;  Score 30;  DB 9;  Length 3328;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy       1 gcggcgtttgagtccgccattggcaagctg 30
           ||||||||||||||||||||||||||||||
Db    2421 GCGGCGTTTGAGTCCGCCATTGGCAAGCTG 2392
```

Sequence Comparison H

```
LOCUS       HUMFGF2H                3365 bp    mRNA    linear   PRI 27-APR-1993
DEFINITION  Human fibroblast growth factor receptor (FGFr) transmembrane form
            mRNA, complete cds.
ACCESSION   M34185
VERSION     M34185.1  GI:182531
KEYWORDS    FGF receptor; fibroblast growth factor receptor; transmembrane
            tyrosine kinase.
SOURCE      Human umbilical vein endothelial cell line HUVEC, cDNA to mRNA,
            clone h2.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3365)
AUTHORS **Johnson,D.E., Lee,P.L., Lu,J. and Williams,L.T.**
TITLE **Diverse forms of a receptor for acidic and basic fibroblast growth factors**
JOURNAL **Mol. Cell. Biol. 10, 4728-4736 (1990)**
MEDLINE 90355989
COMMENT Draft entry and computer-readable sequence for [Unpublished (1990)]
kindly submitted
by D.E.Johnson, 10-MAY-1990.
Author address: D.E.Johnson
University of California San Francisco
4th and Parnassus
Howard Hughes Medical Institute
San Francisco, CA 94143
(415) 476-4297.

FEATURES Location/Qualifiers
source 1. .3365
/organism="Homo sapiens"
/db_xref="taxon:9606"
CDS 256. .2457
/note="fibroblast growth factor receptor (FGFr) transmembrane form"
/codon_start=1
/protein_id="AAA35836.1"
/db_xref="GI:182532"

/translation="MWSWKCLLFWAVLVTATLCTARPSPTLPEQDALPSSEDDDDDDD
SSSEEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWL
KNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVE
RSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPY
VQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLEALEER
PAVMTSPLYLEIIIYCTGAFLISCMVGSVIVYKMKSGTKKSDFHSQMAVHKLAKSIPL
RRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLG
KPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIG
KHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQLSS
KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHHIDYYK
KTTNGRLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLL
KEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEYLDLSM
PLDQYSPSFPDTRSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR"
BASE COUNT 786 a 962 c 917 g 700 t
ORIGIN

Query Match 100.0%; Score 30; DB 9; Length 3365;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 gcggcgtttgagtccgccattggcaagctg 30
          ||||||||||||||||||||||||||||||
Db   2454 GCGGCGTTTGAGTCCGCCATTGGCAAGCTG 2425
```

WEST Search History

DATE: Tuesday, October 29, 2002

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT; PLUR=YES; OP=AND			
L15	l1 and L14	3	L15
L14	l12 and L13	48	L14
L13	philip.in.	16090	L13
L12	barr.in.	856	L12
L11	l1 and L10	2	L11
L10	l8 and L9	31	L10
L9	pablo.in.	274	L9
L8	valenzuela.in.	87	L8
L7	l1 and l6	2	L7
L6	l4 and L5	2	L6
L5	keifer.in.	19	L5
L4	michael.in.	99349	L4
L3	L2 and composition	53	L3
L2	L1 and polynucleotide	55	L2
L1	human adj fibroblast adj growth adj factor	111	L1

END OF SEARCH HISTORY